TO62TO"4ST2Z69

Figure 1

a.

$E_{CTA}M_{AGG}113$

```
                    CTAF
ALLELE 1: 1   TTAAAGGGATATGTTTTTTTCACTAATG-CtGTAAAAATTCACCC--AgATTTTTGCATTTTctttgaaaaaatgt
              ||||||||||||||||||||||||||| | |||||||||||||| | ||||||||||||
ALLELE 2: 1   TTAAAGGGATATGTTTTTTTCACTAATGtC-GTAAAAATTCACCCcaA-ATTTTTGCATTTT--------------

                                                          CTAR
ALLELE 1: 74   tagatatATCATGTTTTTTTACAAGCATTACAATAATATTCACTCGTATATTAGGAATTC 133
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ALLELE 2: 61   -------ATCATGTTTTTTTACAAGCATTACAATAATATTCACTCGTATATTAGGAATTC 113
```

$E_{CCG}M_{AAC}405$

```
                        A2D8F
ALLELE1:  1  TTAAAACCTTGCGTGTGATCGGTATTACAGTACGCAGGGCCA-----------ATCAACTAAAATA-TcTGCA
             |||||||||||||||||||||||||||||||||||||||||           |||||||||||||| | ||||
ALLELE2:  1  TTAAAACCTTGCGTGTGATCGGTATTACAGTACGCAGGGCCAtggtttgagccaATCAACTAAAATAtT-TGCA

                                                          A2D8R
ALLELE1: 62  AACGATAATATAATTATAAGAAAAAGAC-aCACTTTGAGGGCATTTTTGACTTGAGAGAACTCAGGTATCAATCTAA
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
ALLELE2: 74  AACGATAATATAATTATAAGAAAAAGACt-CACTTTGAGGGCATTTTTGACTTGAGAGAACTCAGGTATCAATCTAA

ALLELE1: 138 AAGCAACGCTGTTCACCTTGAGCTGAAACACCTGGAGGAGAAAGCAAAGCAAACCAAACGCGAGAGAGAAATAAAG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ALLELE2: 150 AAGCAACGCTGTTCACCTTGAGCTGAAACACCTGGAGGAGAAAGCAAAGCAAACCAAACGCGAGAGAGAAATAAAG

                        MICROSATELLITE
ALLELE1: 214 AACGGAAACagagAGAGAGAGAGGAAGGACCTTGTTCAAAGCAACGGGGACAACTTTAGAGCCCTGGCGCGCGTGGG
             |||||||||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ALLELE2: 226 AACGGAAAC----AGAGAGAGAGGAAGGACCTTGTTCAAAGCAACGGGGACAACTTTAGAGCCCTGGCGCGCGTGGG

ALLELE1: 291 GGTCAATAAGCGTAACCTGGCTGAGGAGAGCCTCGGCG-tCGTCCTTGCTGAAGCAGAAGAGGAAGAG-CaCGAGA
             |||||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||| | |||||
ALLELE2: 299 GGTCAATAAGCGTAACCTGGCTGAGGAGAGCCTCGGCGc-CGTCCTTGCTGAAGCAGAAGAGGAAGAGcC-CGAGA

ALLELE1: 365 CCAAGAGAAACTCCTCGGAAGCAACGGGAATTC 397
             |||||||||||||||||||||||||||||||
ALLELE2: 373 CCAAGAGAAACTCCTCGGAAGCAACGGGAATTC 405
```

$E_{CGG}M_{AGA}116$

```
ALLELE 1: 1   GAATTCcGGTTATCTCAGACAACTTTTGTTTGGTTTGGTTATAGTAAAGACACGATTAT
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
ALLELE 2: 1   GAATTCtGGTTATCTCAGACAACTTTTGTTTGGTTTGGTTATAGTAAAGACACGATTAT

ALLELE 1: 60  CCAGGCTTTGAGAGGCATAGAAATAATTTTTTTTATATaaAAAAAAAAAGTCTCTTTAA
              |||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
ALLELE 2: 60  CCAGGCTTTGAGAGGCATAGAAATAATTTTTTTTATAT--AAAAAAAAAGTCTCTTTAA
```

$E_{ATG}M_{CGA}87$

```
Allele 1: 1 GAATTCATGGTTTCTCTTAT-----GACATTGTTGCCAAGTAATACTACTATATAAATTCAGATTTGGGTTT
            ||||||||||||||||||||     ||||||||||||||||||||||||||||||||||||||||||||
Allele 2: 1 GAATTCATGGTTTCTCTTATcttatGACATTGTTGCCAAGTAATACTACTATATAAATTCAGATTTGGGTTT

Allele 1: 68  CTGATAACCGTGGTCGTTAA 87
              ||||||||||||||||||||
Allele 2: 73  CAGATAACCGTGGTCGTTAA 92
```

$E_{CCC}M_{ATG}161$

```
ALLELE1: 1 TTAAATGAAAATCGATCAAAATCAAATAATATATGCTTTTTTTAGTTG-gGTTCAAGT-ACT
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |||
ALLELE2: 1 TTAAATGAAAATCGATCAAAATCAAATAATATATGCTTTTTTTAGTTGt-GTTCAAGTaACT

ALLELE1: 61 TTTTTTTATTGAAAAAATCGACCCAAGTTGAAACACATGTTTGAGAATTGTTTTGT 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ALLELE2: 62 TTTTTTTATTGAAAAAATCGACCCAAGTTGAAACACATGTTTGAGAATTGTTTTGT 117

ALLELE1: 117 GCATCCAACGTTTTTCTTGTACAATCAGCTGTGAGAGGGGAATTC 161
             |||||||||||||||||||||||||||||||||||||||||||
ALLELE2: 118 GCATCCAACGTTTTTCTTGTACAATCAGCTGTGAGAGGGGAATTC 162
```

$E_{CCA}M_{AGC}114$

```
ALLELE1: 1 GAATTCCCAGcC-AGATTTGTATCAAACATGTATTGTCCACAAAATGTTCAAGCATCTTA 59
           |||||||||| | ||||||||||||||||||||||||||||||||||||||||||||
ALLELE2: 1 GAATTCCCAG-CtAGATTTGTATCAAACATGTATTGTCCACAAAATGTTCAAGCATCTTA 59

ALLELE1: 60 GGGAACTGCTATTCTTACTTCTAAATTTTTTATTGACATCCAAAGTGTGCTTTAA 114
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
ALLELE2: 60 GGGAACTGCTATTCTTACTTCTAAATTTTTTATTGACATCCAAAGTGTGCTTTAA 114
```

b.

$E_{ATG}M_{CGA}87$ BAC extension and TaqMan probe and primers

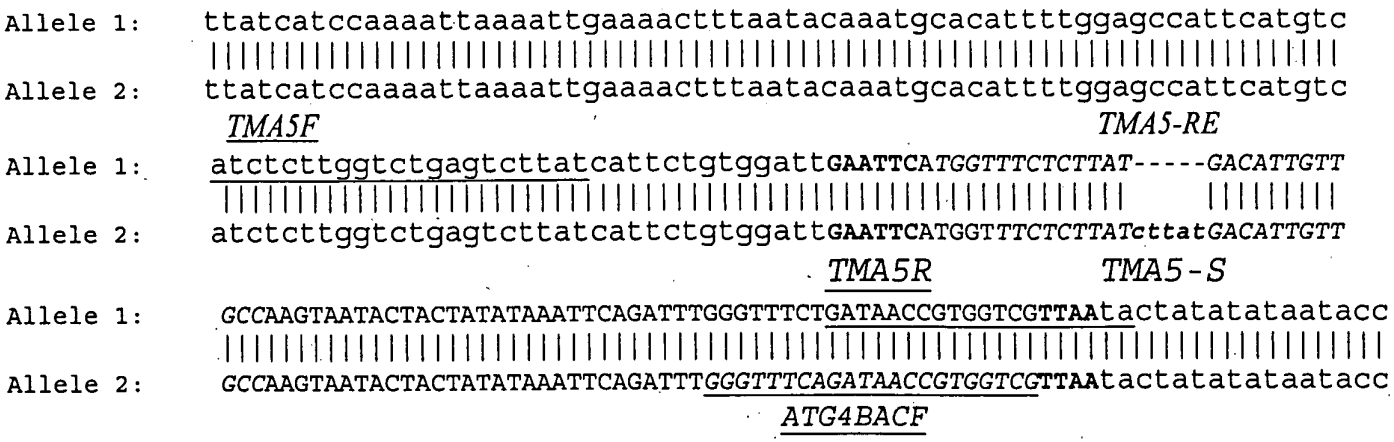


Figure 2

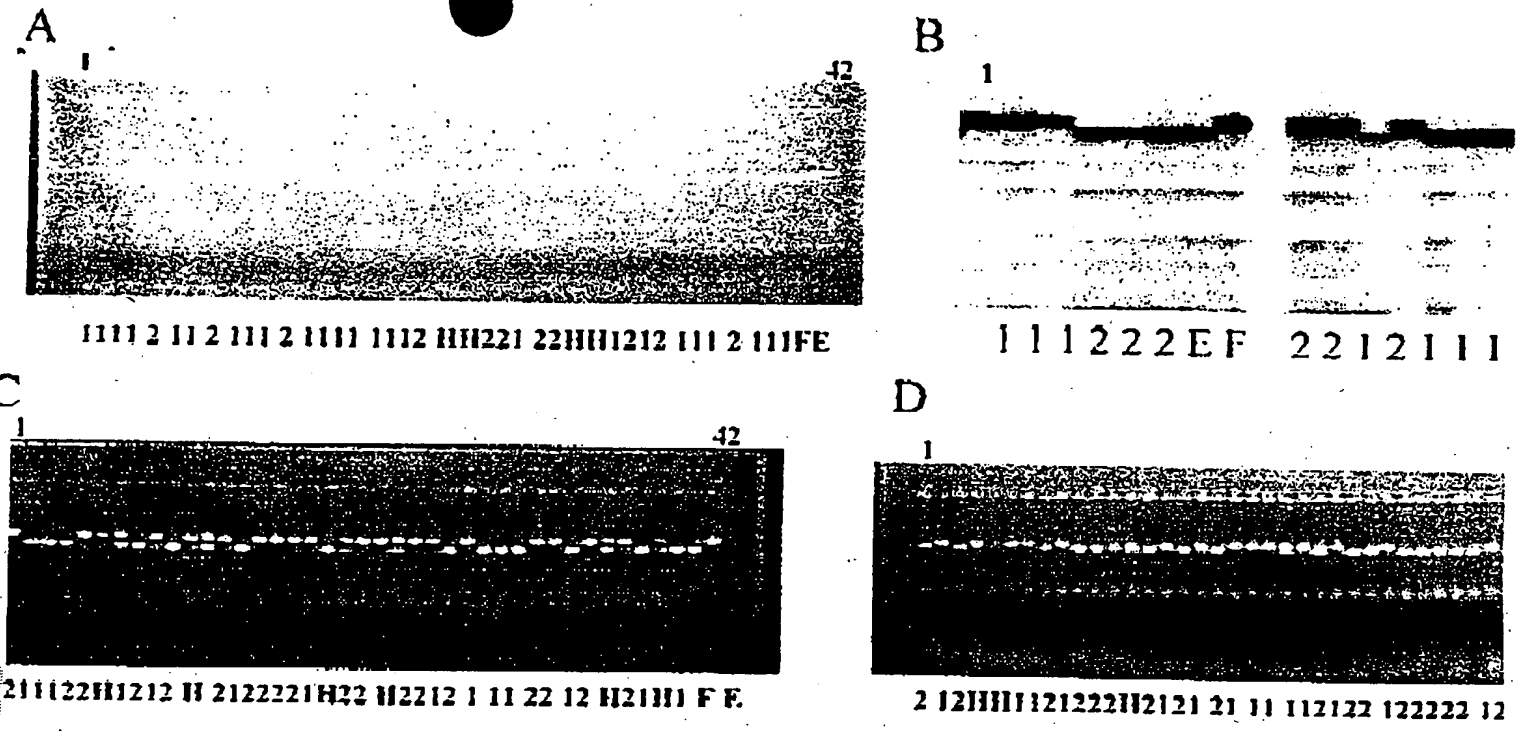


Figure 3

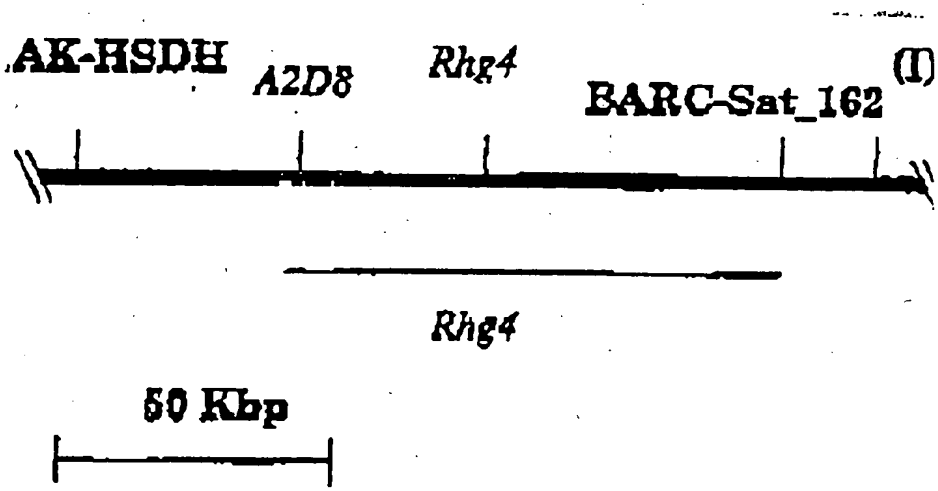


Figure 4

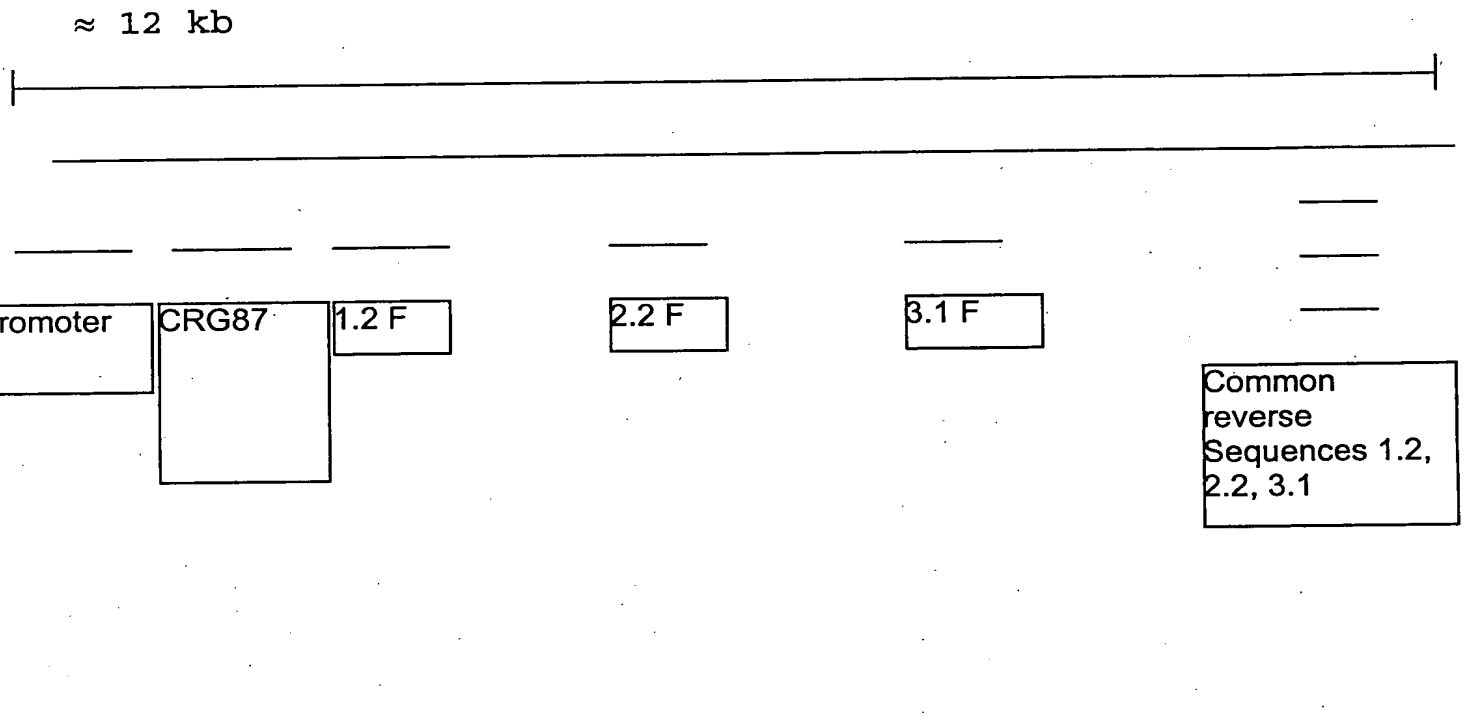
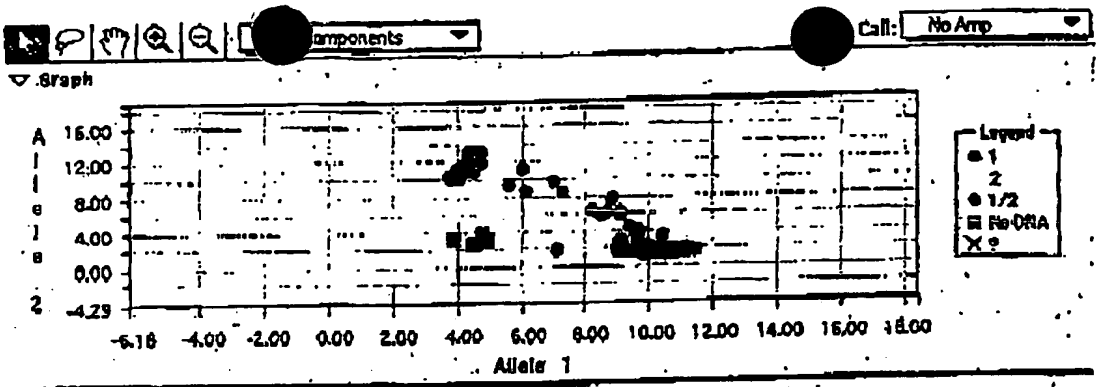

≈ 12 kb
Promoter
CRG87
1.2 F
2.2 F
3.1 F
Common reverse Sequences 1.2, 2.2, 3.1

Figure 5



Panel A

Plate

Tray

	1	2	3	4	5	6	7	8	9	10	11	12
A	1	2	1	2	1	1	2	2	1	2	1	2
B	2	1	1	1	1 and 2	1	1	1	1	2	1	2
C	1	1	2	1	1	2	1	2	2	1	1	1
D	1	1	2	2	2	1	2	2	1	1	1	1
E	No Amp	1	2	1	1	No Amp	1	1 and 2	2	1	1	No Amp
F	1	1	1	1	1	1	1	1	2	2	2	No Amp
G	2	1	1 and 2	1	2	1	1	1	1	1	1	No Amp
H	1	1	1	1	1	1	1	2	1	1 and 2	1 and 2	

Panel B

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Figure 6

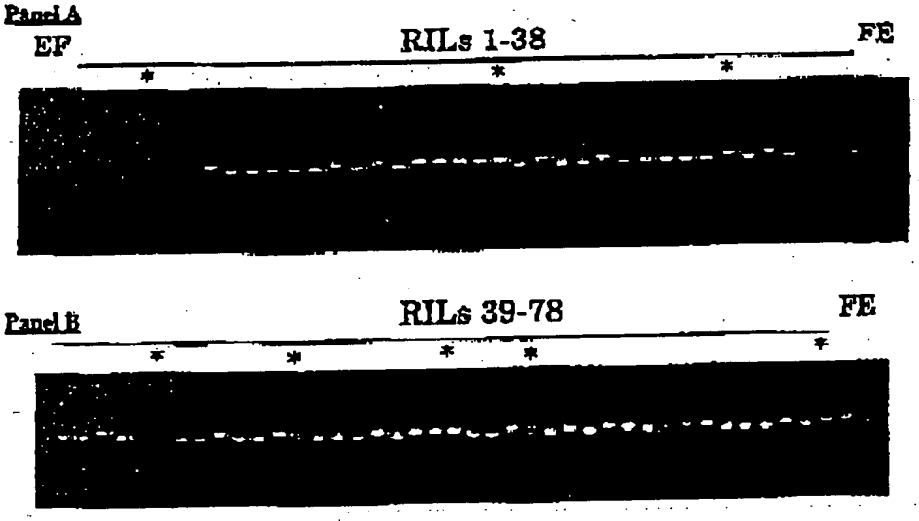

Figure 7A

Synthetic rhg1 gene

1

AATGGGAGGAGTGGGAAAGACAGTGGCTATGGAGCTTGTTCCGGAGGTTGGGTTGGAAT
CAAGTGTGCTCAGGGACAGGTTATTGTGATCCAGCTTCCTTGGAAGGGTTTGAGGGGTC
GAATCACCGACAAAATTGGCCAACTTCAAGGCCTCAGGAAGCTTAGTCTTCATGATAAC
CAAATTGGTGGTTCAATCCCTTCAACTTTGGGACTTCTTCCCAACCTTAGAGGGGTTCA
GTTATTCAACAATAGGCTTACAGGTTCCATACCTCTTTCTTTAGGTTTCTGCCTTTGCT
TCAAGTCTCTTGACCTCAGCAACAACTTGCTCACAGGAGCAATCCCTTATAGTCTTGCT
AATTCCACTAAGCTTTATTGGCTTAACTTGAGTTTCAACTCCTTCTCTGGTCCTTTACC
AGCTAGCCTAACTCACTCATTTTCTCTCACTTTTCTTTCTCTTCAAAATAACAATCTTT
CTGGCTCCCTTCCTAACTCTTGGGGTGGGAATTCCAAGAATGGCTTCTTTAGGCTTCAA
AATTTGATCCTAGATCATAACTTTTTCACTGGTGACGTTCCTGCTTCTTTGGGTAGCTT
AAGAGAGCTCAATGAGATTTCCCTTAGTCATAATAAGTTTAGTGGAGCTATACCAAATG
AAATAGGAACCCTTTCTAGGCTTAAGACACTTGACATTTCTAATAATGCCTTGAATGGG
AACTTGCCTGCTACCCTCTCTAATTTATCCTCACTTACACTGCTGAATGCAGAGAACAA
CCTCCTTGACAATCAAATCCCTCAAAGTTTAGGTAGATTGCGTAATCTTTCTGTTCTGA
TTTTGAGTAGAAACCAATTTAGTGGACATATTCCTTCAAGCATTGCAAACATTTCCTCG
CTTAGGCAGCTTGATTTGTCACTGAATAATTTCAGTGGAGA**AATTCCAG**TCTCCTTTGA
CAGTCAGCGCAGTC**TAAAT**CTCT**TCA**ATGTTTCCTACAATAGCCTCTCAGGTTCTGTCC
CCCCTCTGCTTGCCAAGAAATTTAACTCAAGCTCATTTGTGGGAAATATTCAACTATGT
GGGTACAGCCCTTCAACCCCATGTCTTTCCCAAGCTCCATCACAAGGAGTCATTGCCCC
ACCTCCTGAAGTGTCAAAACATCACCATCATAGGAAGCTAAGCACCAAAGACATAATTC
TCATAGTAGCAGGAGTTCTCCTCGTAGTCCTGATTATACTTTGTTGTGTCCTGCTTTTC
TGCCTGATCAGAAAGAGATCAACATCT**AGGCCGGG**AACGGCCAAGCCACCCGAGGGTAG
AGCGGCCACTATGAGGACAGAAAAAGGAGTCCCTCCAGTTGCTGGTGGTGATGTTGAAG
CAGGTGGGGAGGCTGGAGGGAAACTAGTCCATTTTGATGGACCAATGGCTTTTACAGCT
GATGATCTCTTGTGTGCAACAGCTGAGATCATGGGAAAGAGCACCTATGGAACTGTTTA
TAAGGCTATTTTGGAGGATGGAAGTCAAGTTGCAGTAAAGAGA**TTGAGGGAAAAGAT**CA
CTAAAGGTCATAGAGAATTTGAATCAGAAGTCAGTGTTCTAGGAAAAATTAGACACCCC
AATGTTTTGGCTCTGAGGGCCTATTACTTGGGACCCAAA**GGGGAAAA**GCTTCTGGGTTT
TGATACATGTCTAAAGGAAGTCTTGCTTCTTTCCTACATGGAAGGTTCGTGTGCTGGTT
CTTTCATTAAAGTGTTGTGTGTGCTGGTCTTTAATTATAATTTGGAGTTTTACCTTAGT
AATCTGTATAATTCTAATCGGAGAACAGTACAAACAAAAACACCTAAGGAACAACACCT
TANCTTTAATATACCATATCAATAAAGTGAAATATTTTCTTGGTCATCTTGATGCAGGG
GGAACTGAACATTCATTATTGGCCACAA**GATTAAAAT**AGCCCAAGCCTTGGCCCGGGCT
TGTTTGCCTTCATTCCCAGGAGAACATCATACATGGGACCTCNCATCCAGCAATGTGTG
GCTTGATGAAAAACAAATGCTAAAATTCAGATTTTGGTCTTTTTCGGGTTGATGTCAAC
TGCTGCTAATTCCAACGTGATAGCTACAGCTGGAGCATTGGATACCGGGCACCTGAGCT
CTCAAAGCTCAAGAAAGCAAACACTAAAACTGATATCTACAGTCTTGGTGTTATCTTGT
TAGAACTCCTAACGAGGAAATCACCTGGGGTGTCTATGAATGGACTAGATTTGCCTCAG
TGGGTTGCCTCAGTTGTCAAAGAGGAGTGGACAAATGAGGTTTTTGATGCAGACTTGAT
GAGAGATGCATCCACAGTTGGCGACGAGTTGCTAAACACGTTGAAGCTCGCTTTGCACT
GTGTTGATCCTTCTCCATCAGCACGACCAGAAGTTCATCAAGTTCTCCAG**CAGCTGAAG**
AGATTAGACCAGAGAGATCAGTCACAGCCAGTCCCGGGGACGATATCGTATAGCACAAA
TTTTGCATTGATTTTTTTGTGCCAAATGTAGTAGGCCTACTATATATATGTTCTATGAT

Figure 7B

TCTTTCATTCTTATATTATTTTTGCCTGTTTGAATGCTTGAATTTGTACATACTCATAC
TACAATAAGGTGTAGTTCTGGTTAATTTTACCTCTACCTCAAAGCTGGGGTGTAATTCT
GTTTCCTCCAAGGCACATAATAGTTGAAAATAGTTCTCAGGAGCATTCATTGTTTATTC
TGCAAGATTCTCTTTCACGGCTGCTATCTTCTATGCATGCCCTGCCCA**TAAAT**GCATTA
TGAAGAATTGTAACGGCTGTGTTTTTGGACTTCTTCAAAAAGTTTATGTTATTGCCAGG
TGTATATATCAACATGTTTTAAAGATTTTCAAACAATCAGGTTTTAGATGTGGGTTTGC
ATGCATGAGATTGGACTAGTGCGCTTGATGTAGTATAAAATA**TAAAT**TGTCCAATCAAG
CACCCTCTACATGTCCAAATAATGGGCCTTATGAAACTTAATTTTTTAATTACAAACTA
CAGTAATCTTTTTGAATAAAGATTTACAAATTACAACNGACATGTGAAGCNGCATCTTT
NATTGNCAATCTTTCAAGTTACTCTATTATTTTCTGCN

3105bp

PCT/US2004/000000

Figure 7C

Rhg1 Peptide
NGRSGKDSGYGACSGGWVGIKCAQGQVIVIQLPWKGLRGRIT
DKIGQLQGLRKLSLHDNQIGGSIPSTLGLLPNLRGVQLFNNRLG
SIP
LSLGFCPLLQSLDLSNNLLTGAIP
YSLANSTKLYWLNLSFNSFSGPLP
ASLTHSFSLTFLSLQNNNLSGSLPNSWGG
NSKNGFFRLQNLILDHNFFTGDVP
ASLGSLRELNEISLSHNKFSGAIP
NEIGTLSRLKTLDISNNALNGNLP
ATLSNLSSLTLLNAENNLLDNQIP
QSLGRLRNLSVLILSRNQFSGHIP
SSIANISSLRQLDLSLNNFSGEIP
VSFDSQRSLNLSNVSYNSLSGSVP

PLLAKKFNSSSFVGNIQLCGYSP
STPCLSQ
APSQGVIAPPPEVSKHHHHR
KLSTKDIILIVAGVLLVVLIILCCVLLFCLIRKRS
TSKAGNGQATEGRAATMRTEKGVPPVAGGDVEAGGEAGGKLVHF
DGPMAFTADDLLCATAEIMGKSTYGTVYKAILEDGSQVAVKRLR
EKITKGHREFESEVSVLGKIRHPNGLALRAYYLGPKGEKLLVFD
YMSKGGLLLFYMEGSCAGSFIKVLCVLVFNYNLEFYLSNLYNSN
RRTVQTKTPKEQHLXFNIPYQ
-SEIFSWSS-CRGN-TFIIGHKMKIXQDLAVACSPSFPETSYMD
LXSSNVCX-NXMLKLQFWSFSVDVNCC-FQRDSYSWSIGIPGT-
ALKAQESKH-N-YLQSWCYLVRTPNEEITWGVYEWTRFASVGCL
SCQRGVDK-GF-CRLDERCIHSWRRVAKHVEARFALC-SFSIS
TTRSSSSSPAAGRD-TREISHSQSHLPGRPLEPYSESY

Sequence Listing - Page 1 of 1

Figure 7D

Sequences producing significant alignments:	Score (bits)	E Value
pir:T46070 hypothetical protein T18N14.120 - Arabidopsis thaliana	632	e-180
pir:T47727 hypothetical protein F18O21.60 - Arabidopsis thaliana	344	1e-95
pir:T04587 hypothetical protein F23E13.70 - Arabidopsis thaliana	268	9e-71
pir:T49038 hypothetical protein T5P19.20 - Arabidopsis thaliana	257	2e-67
pir:T48210 hypothetical protein T20L15.160 - Arabidopsis thaliana	241	1e-62
pir:T05050 protein kinase homolog M3E9.30 - Arabidopsis thaliana	238	2e-61
pir:T18536 receptor-like protein kinase - Ipomoea nil (Japanese...	236	3e-61
pir:T48489 receptor-like protein kinase - Arabidopsis thaliana	236	5e-61
pir:T10515 disease resistance protein Cf-2.2 - currant tomato	235	6e-61
pir:T10504 disease resistance protein Cf-2.1 - currant tomato	235	6e-61
pir:T30553 disease resistance protein Hcr2-5D - tomato	229	4e-59
pir:S27756 receptor-like protein kinase 5 (EC 2.7.1.-) precurso...	227	1e-58
pir:T48499 receptor-like protein kinase-like protein - Arabidop...	226	3e-58
pir:T46033 receptor protein kinase-like protein - Arabidopsis t...	226	4e-58
pir:T05335 hypothetical protein F1C12.190 - Arabidopsis thaliana	221	1e-56
pir:T10636 hypothetical protein T13K14.100 - Arabidopsis thaliana	219	7e-56
pir:T05898 hypothetical protein F6H11.170 - Arabidopsis thaliana	218	1e-55
pir:T45717 receptor-kinase like protein - Arabidopsis thaliana	212	7e-54
pir:T05322 hypothetical protein F18F4.240 - Arabidopsis thaliana	211	1e-53
pir:T10659 probable serine/threonine-specific protein kinase (E...	211	2e-53
pir:T03784 probable receptor protein kinase - rice	208	1e-52
pir:T50851 receptor protein kinase homolog [imported] - soybean	201	1e-50
pir:T45647 receptor protein kinase-like protein - Arabidopsis t...	199	5e-50
pir:T45718 receptor-kinase like protein - Arabidopsis thaliana	199	7e-50
pir:T50850 receptor protein kinase homolog [imported] - soybean	199	7e-50
pir:T45645 receptor kinase-like protein - Arabidopsis thaliana	196	3e-49
pir:T09356 brassinosteroid-insensitive protein BRI1 - Arabidops...	196	3e-49
pir:T00712 protein kinase homolog F22O13.7 - Arabidopsis thaliana	190	2e-47
pir:A57676 protein kinase Xa21 (EC 2.7.1.-), receptor type prec...	190	3e-47
pir:S39476 kinase-like transmembrane protein TMKL1 precursor - ...	188	1e-46
pir:T02154 protein kinase homolog T1F15.2 - Arabidopsis thaliana	188	1e-46
pir:T10725 protein kinase Xa21 (EC 2.7.1.-) A1, receptor type -...	186	5e-46
pir:T05897 protein kinase homolog F6H11.160 - Arabidopsis thaliana	184	1e-45
pir:T04313 protein kinase Xa21 (EC 2.7.1.-), receptor type - rice	183	3e-45
pir:T10727 protein kinase Xa21 (EC 2.7.1.-) D, receptor type - ...	181	2e-44

Figure 7E

```
>pir:T46070 hypothetical protein T18N14.120 - Arabidopsis thaliana
            Length = 836

 Score =  632 bits (1613), Expect = e-180
 Identities = 329/550 (59%), Positives = 400/550 (71%), Gaps = 2/550 (0%)
 Frame = +1

Query: 7    RSGKDSGYGACSGGWVGIKCAQGQVIVIQLPWKGLRGRITDKIGQLQGLRKLSLHDNQIG 186
             +S  +S       GW GIKC +GQV+ IQLPWKGL G I++KIGQL  LRKLSLH+N I
Sbjct: 72   KSWNNSASSQVCSGWAGIKCLRGQVVAIQLPWKGLGGTISEKIGQLGSLRKLSLHNNVIA 131

Query: 187  GSIPSTLGLLPNLRGVQLFNNRLTGSIPLSLGFCLCFKSLDLSNNLLTGAIPYSLANSTK 366
             GS+P +LG L +LRGV LFNNRL+GSIP+SLG C    ++LDLS+N LTGAIP SL  ST+
Sbjct: 132  GSVPRSLGYLKSLRGVYLFNNRLSGSIPVSLGNCPLLQNLDLSSNQLTGAIPPSLTESTR 191

Query: 367  LYWLNLSFNSFSGPLPASLTHSFSLTFLSLQNNNLSGSLPNSWGGNSKNGFFRLQNLILD 546
             LY LNLSFNS SGPLP S+  S++LTFL LQ+NNLSGS+P+ +     NG   L+ L LD
Sbjct: 192  LYRLNLSFNSLSGPLPVSVARSYTLTFLDLQHNNLSGSIPDFF----VNGSHPLKTLNLD 247

Query: 547  HNFFTGDVPASLGSLRELNEISLSHNKFSGAIPNEIGTLSRLKTLDISNNALNGNLPATL 726
             HN F+G VP SL     L E+S+SHN+ SG+IP E G L  L++LD S N++NG +P +
Sbjct: 248  HNRFSGAVPVSLCKHSLLEEVSISHNQLSGSIPRECGGLPHLQSLDFSYNSINGTIPDSF 307

Query: 727  SNLSSLTLLNAENNLLDNQIPQSLGRLRNLSVLILSRNQFSGHIPSSIANISSLRQLDLS 906
             SNLSSL  LN E+N L   IP ++ RL NL+ L L RN+ +G IP +I NIS +++LDLS
Sbjct: 308  SNLSSLVSLNLESNHLKGPIPDAIDRLHNLTELNLKRNKINGPIPETIGNISGIKKLDLS 367

Query: 907  LNNFSGEIPVSFDSQRSLNLFNVSYNSLSGSVPPLLAKKFNSSSFVGNIQLCGYSPSTPC 1086
              NNF+G IP+S      L+ FNVSYN+LSG VPP+L+KKFNSSSF+GNIQLCGYS S PC
Sbjct: 368  ENNFTGPIPLSLVHLAKLSSFNVSYNTLSGPVPPVLSKKFNSSSFLGNIQLCGYSSSNPC 427

Query: 1087 LSQAPSQGVIAPP--PEVSKHHHHRKLSTKDIILIVAGVLLVVLIILCCVLLFCLIRKRS 1260
              +      +   P   +  + HHHRKLS KD+ILI  G LL +L++LCC+LL CLI+KR+
Sbjct: 428  PAPDHHHPLTLSPTSSQEPRKHHHRKLSVKDVILIAIGALLAILLLLCCILLCCLIKKRA 487

Query: 1261 TSRPGTAKPPEGRAATMRTEKGVPPVAGGDVEAGGEAGGKLVHFDGPMAFTADDLLCATA 1440
                 K  +G+  T  +EK V     G   AGGE GGKLVHFDGP  FTADDLLCATA
Sbjct: 488  -----ALKQKDGKDKT--SEKTVSAGVAGTASAGGEMGGKLVHFDGPFVFTADDLLCATA 540

Query: 1441 EIMGKSTYGTVYKAILEDGSQVAVKRLREKITKGHREFESEVSVLGKIRHPNVLALRAYY 1620
             EIMGKSTYGT YKA LEDG++VAVKRLREK TKG +EFE EV+ LGKIRH N+LALRAYY
Sbjct: 541  EIMGKSTYGTAYKATLEDGNEVAVKRLREKTTKGVKEFEGEVTALGKIRHQNLLALRAYY 600

Query: 1621 LGPKGEKLLGFD 1656
             LGPKGEKLL FD
Sbjct: 601  LGPKGEKLLVFD 612
```

Figure 7F

```
 Score =  185 bits (464), Expect = 1e-45
 Identities = 93/161 (57%), Positives = 122/161 (75%), Gaps = 3/161 (1%)
 Frame = +2

Query: 1943 GLVCLHSQENIIHGTSHPAMCGLMKNKC*NS---DFGLFRVDVNCC*FQRDSYSWSIGYR 2113
          GL  LHS EN+IH   +     ++ ++  N+   D+GL R+           + + ++GYR
Sbjct: 647  GLAHLHSNENMIH--ENLTASNILLDEQTNAHIADYGLSRLMTAAAATNVIATAGTLGYR 704

Query: 2114 APELSKLKKANTKTDIYSLGVILLELLTRKSPGVSMNGLDLPQWVASVVKEEWTNEVFDA 2293
          APE SK+K A+ KTD+YSLG+I+LELLT KSPG   NG+DLPQWVAS+VKEEWTNEVFD
Sbjct: 705  APEFSKIKNASAKTDVYSLGIIILELLTGKSPGEPTNGMDLPQWVASIVKEEWTNEVFDL 764

Query: 2294 DLMRDASTVGDELLNTLKLALHCVDPSPSARPEVHQVLQQLKRL 2425
          +LMR+  +VGDELLNTLKLALHCVDPSP+ARPE +QV++QL+ +
Sbjct: 765  ELMRETQSVGDELLNTLKLALHCVDPSPAARPEANQVVEQLEEI 808
```

Document #: 2004-0004